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Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd.
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ALIGNMENTS

RESULT 1 09U5H1 PRELIMINARY: PRT; 458 AA. 1D 09U5H1; DT 01-MAY-2000 (TrEMBLrel. 13, Careated) DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-MAY-2000 (TrEMBLrel. 19, Last annotation update) DT 01-MAY-2000 (TrEMBLrel. 19, Last annotation update) DE 48UDA MECOZOTTE ANTIGEN. SPECHON N. A. REC EMBATYOTA; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia caballi. OS Babesia caballi. OS RABOSA; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia CRELITARID-5871; RN [1] RN [2]																			
CCC update) (CCC u	61 61	– –	100.0%; 100.0%; vative 0;	Merozoite. SEQUENCE 458 AA; 52138 MW;									48KDA MEROZOITE ANTIGEN.	01-DEC-2001 (TremBirel, 19,	01-MAY-2000 (TrEMBLrel. 13,	Q9U5H1;	9U5H1 PRELIMINARY;	RESULT 1	
→			Length 458; Indels 0;	66AF2D CRC64;		recombinant antigen in an	n Babesia caballi merozoite	., Kamemaru T., Nagasawa H.,			asmida; Babesiidae; Babesia.			on update)			AA.		

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"Detection of equine antibodies to tabesia caballi caballi rhoptry-associated protein in a competiti enzymanishkod immunsagothent assay."

Colin. Microbiol. 37.7365-2290(1999).
EMBL; AF092736; AAD40991.1;

InterPro; IPR004318; RAP-1.
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CIATED PROTEIN-1.
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MCElwain T.F.;
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Submitted (OCT-1997) to the EMBL; AF037149; AAC27387.1; --

R EMBL; AF030054; AAB84264.1; --

R EMBL; AF030055; AAB84265.1; --

R EMBL; AF030059; AAB84265.1; --

R EMBL; AF030059; AAB84269.1; --

R EMBL; AF03019; AAC27386.1; --

R EMBL; AF03019; AAB84269.1; --

R EMBL; AF030059; AB84269.1; --

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R EMBL; AF030059; AAB84269.
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STRAIN-MEXICO MO7;
STRAIN-MEXICO MO7;
MEDLINE-98327208; PubMed-9662706;
Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.;
"Structure, sequence, and transcriptional analysis bovis rap-1 multigene locus.";
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Suarez C.E., Palmer G.H.,
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R EMBL; M38218; AAA62695.1; -.

R Interpro; IPR004318; RAP-1.
Pfam; PF03085; RAP-1; 1.
SEQUENCE 565 AA; 64076 ...
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01-NOV-1996
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STRAIN-MO7; TISSUE-LAMBDA-ZAP II LAMBDA-GT11;
MEDLINE-91304520; PubMed-1712911;
Suarez C.E., Palmer G.H., Jasmer D.P., Hines
MCELwain T.F.;
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Babesia bovis
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Suarez C.E., I
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Suarez C.E., Palmer G.H.,
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Pred. No. 1.4e
79; Mismatches
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                                                                                                                                                                                                                                            Piroplasmida; Babesiidae;
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                                    InterPro; 1FAVE.

Pfam; PF03085; F
Pfam; PF03085; F
                                     Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.; "Structure, sequence, and transcriptional analysis of the bovis rap-1 multigene locus."; Submitted (CCT-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF030057; AAB84267.1; -. InterPro; IPR00431B; RAP-1. 1. Pfam; PF030085; RAP-1; 1. Pfam; PF030085; RAP-1; 1. SEQUENCE 565 AA; 64906 MW; 5A60A059E931D3B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-1997) to the EMBL; AF030056; AAB64266.1; InterPro; IPR004318; RAP-1. Pfam; PF03085; RAP-1; 1. SEQUENCE 565 AA; 64934 MV
                                                                                                                                                                              Babesia bovis.
Eukaryota; Alveolata;
NCBI_TaxID=5865;
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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Pred. No. 1.4
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Query Match
Best Local :
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"Structure, sequence, and transcriptional analysis of the
bovis rap-1 multigene locus.";

submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF030062; AAB42772.1;

InterPro; IPR004318; RAP-1.

Pfam; PF03085; RAP-1; 1.

SEQUENCE 565 AA; 64979 MW; 7F5E0019DEBA1892 CRC64;
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01-DEC-2001
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01-MAY-2000
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STRAIN-R1A;
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                                                                                                                                                                                Similarity
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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36.5%;
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                                                                                                                                                                                Score 825.5; DB 5
Pred. No. 1.6e-46;
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                                                                                                                                                             Mismatches
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01-NOV-1996
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Q17126;
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InterPro; IPR00431B; RAP-1.
Pfam; PF03085; RAP-1; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SEQUENCE 456 AA; 52470 MW; 87C57CA40A8DB924 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterisation of a family of multi-copy genes protein homologues in Babesia bovis, Babesia ovis Mol. Biochem. Parasitol. 57:181-192(1993).
EMBL; M91168; AAA27807.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-TOWNSVILLE;
MEDLINE-93165069; PubMed-8433711;
Dalrymple B.P., Casu R.E., Peters
Wright I.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Babesia canis
Eukaryota; Alv
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  AFWMRFRHGGRYGAYHNFLVNILYKNLSDSMVDDNLEGFVRKYAYMATMYYKTYTALDVV
                       REWMRERRGKNHSYFHDLVENLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEF 180
                                                                                         KSVAEYVESCVRYDCFSIENQKYPQEKEYQPLTLPNPYQLEAAFYVFRNSESNPIKNPTE
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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                                                                                                                                                                                                                                                                       32.7%; Score 770.5; DB 5; 35.0%; Pred. No. 5.1e-43; tive 95; Mismatches 161;
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EMBL; M91169, AAA27805.1; -.
InterPro; IPR004318; RAP-1.
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Dalrymple B.P., Casu R.E, Peters
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                                                                                                                                                       RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEF
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GPWMRYKEGKEHGDYHHFIISLLGKSLVRKDGVTDLEFLVNKLLYMATTYYKTYLIVKKF
                                                                                                                                                                                                                  ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
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                                       TLSKFAERYSDMVMKVLLSSLAGYVKAPWYKRWINRFKSLLTGEAYNPDEDIHLLKPIFV
                                                               ALPKFAKRESLMVVQRLLATVAGYVDTPWYKKWYMKLKNEMVNR-
                                                                                      GARFFNTFSFTMNIFGIGIKRALKGIVRSNVPEDMG-EHSIERISHLSEGYKDYMLTQVP
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                                                                                                                                                                                                                                                                                               161;
                                                                                                                                                                                                                                                                                                                                                                                                                                      I.G.;
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                               496 AA;
                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKEFFVNKIHEPTKEFFVNKIHEPT----
                                                                                                                                                                                                                                                                                                                                               56892 MW;
                                                                                                                                                                                                                                                                                                       32.2%;
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                                                                                                                                                                                                                                                                                            93;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                        Score 759.5; DB 5;
Pred. No. 3e-42;
                                                                                                                                                                                                                                                                                                                                               2E4020EBD2AF4999 CRC64;
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.M.,
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                                                                                                                                                                                                                                                                                            173;
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and Babesia
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RESULT Q17257 ID Q1 AC Q1

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Q17257 Q17257;

PRELIMINARY;

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321 AA

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Best Local S
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Q17121;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RHOPTRY ASSOCIATED PROTEIN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03085; RAP-1;
NON_TER 1
SEQUENCE 445 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suarez C.E., Palmer G.H., Hines S.A., McElwain T.F.;
"The Babesia bovis rhoptry associated protein-1 intergenic encodes a functional eukaryotic promoter.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; L77326; AAA96414.1; ...
InterPro; IPR004318; RAP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesia bovis.
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-MO7;
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LPLDIGTEHSVSRLQHITSSYKDYMDTQIPALPKFAKRESLMVVQRLLATVAGYVDTPWY 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVKNDLLDAVN--IRNILRGSSQDDNNEQEKTEEEKVEEVKPELKQKEYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTPRNYIKDALKPLRDAVEENIVNPVSDYLRRKQNISRSQNYNDGHHKIDPSLYEPKRPH 389
                         SKALIRKVYTEADDLFENKIGQGTVDFINKEIRDPSKALIR-KVSTEADNL
                                                     QATKHFLGENIAQPTKEFFKDVPQVTKKVITENIAQPTKEFI
                                                                             QGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDF------INNEIRDP 405
                                                                                                       VAEPTKTFFKEAPQVTKHFFDENIGQPTKEFFREAPQATKHFLDENIGQPTKEFF-REAP
                                                                                                                                                                                       KKWYMKLKNFMVNRVFIPTKKF------
                                                                                                                                                                                                                  VPEDF-EERSIERITQLTSSYEDYMLTQIPTLSKFARRYADMVKKVLLGSLTSYVEAPWY
                                                                                                                                                                                                                                                                                                  ADATDIENFASRYLYMATLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSN 210
                                                                                                                                                                                                                                                                                                                            PLSLPNPYQLDAAFRLFKESASNPAKNSVKREWLRFRNGANHGDYHYFVTGLLNNNVVHE
                                                                                                                                                                                                                                                                                                                                                                                  146;
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                                                                                                                                                             KRWIKKFRDFFSKNVTQPTKKFIEDTNEVTKNYLKANVAEPTKKFMQDTHEKTKGYLKEN
                                                                                                                                                                                                                                                                       EGTTDVEYLVNKVLYMATMNYKTYLTVNSMNAKFFNRFSFTTKIFSRRIRQTLSDIIRWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                    51355 MW;
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                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                               Score 665.5; DB 5;
Pred. No. 4.1e-36;
4; Mismatches 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    3A324715F8DAFB7C CRC64;
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RESULT 16
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Best Local
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Q17255;
Q1-NOV-1996
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01-NOV-1996
01-DEC-2001
            Pfam; PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein homologues in Babesia bovis, Babesia Mol. Biochem. Parasitol. 57:181-192(1993). EMBL: M91173; AAA27811.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveo NCBI_TaxID=5869; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUTATIVE (60.2 OR .3) Babesia ovis.
                                             Mol. Biochem. Parasitol. 57:181-192(1993). EMBL; M91169; AAA27804.1; -.
                                                                                                                                                                                 Babesia ovis
Eukaryota; Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
 SEQUENCE
                                    InterPro
                                                                      "Characterisation of a family of multi-copy genes protein homologues in Babesia bovis, Babesia ovis
                                                                                                         Dalrymple B.P., Casu R.E, Peters J.M., Dimmock C.,
                                                                                                                       MEDLINE-93165069; PubMed-8433711;
                                                                                                                                   STRAIN-ANKARA
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                      NCBI_TaxID=5869;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterisation of a family of multi-copy genes protein homologues in Babesia bovis, Babesia ovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dalrymple B.P., Casu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                             IRDPSKALI-RKVYTEADDLFENKIGQGTVDFINKEIRDPSK 442
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                      PF03085;
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ER 1
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                                   IPR004318; RAP-1.
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                                                                                                                                                                                 Alveolata;
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                                                                                                                                                                                                                                                                   PRELIMINARY;
AA;
                        RAP-1;
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31779
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11. 01, Last sequence update)
11. 19, Last annotation update)
RHOPTRY PROTEIN (FRAGMENT).
                                                                                                                                                                                  Apicomplexa;
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Last annotation update)
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                                                                                                                                                                                                                                                                     PRT;
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BE954830D9EAC399
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                                                                                                                                                                                 Piroplasmida;
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د
CRC64;
                                                                                                                                                                                  Babesiidae;
                                                                     encoding and Babes
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and Babesia cani
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                                                                         Babesia
                                                                                                          K.R,
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                                                                                   rhoptry
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Best Local Similarity
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Q17129;
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                            Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
RHOPTRY ASSOCIATED PROTEIN PRECURSOR.
Babesia divergens.
Eukaryota; Alveelata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004318; RAP-1.
Pfam; PF03085; RAP-1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Skuce P.J., Mallon T.R., Taylor S.M.; "Molecular cloning of the rhoptry associated
                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-DRUMANESS;
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                                                                                                                                                                                                                                                                                                                                                                                                    Babesia divergens."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=32595;
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 ALPKFAKRESLMVVQRLLATVAGYVDTPWYKKWYMKLKNEMVNRVFIPTKKFFNKEIREP
                                                   GASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP
                                                                              NFGMRFKHGGRYGAYQSFIMNVVTSSYTQLSDNTEVEDLVNRYLYMATMYYKTYLILDTT
                                                                                          REWMRERRGKNHSYFHDLVFNLLEKNVTRDADATDIENEASRYLYMATLYYKTYTNVDEF
                                                                                                                                   ESVRTYVSRCIORGCLKIDHERYAAEKGNQPLAFPNPYQVGAAFQLFQECDSDPTQEPNG
                                                                                                                                                    ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
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                           KVHLINKIDFGHHISGKSIKHMVEKIIRNHLPRDFGI-YSIERLSHISAGYGDYILKQVP
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Pred. No. 2.3e-30;
                                                                                                                                                                                                                                                        Score 569.5;
Pred. No. 7.
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RHOPTRY ASSOCIATED PROTEIN
F74440D6F5C1D151 CRC64;
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   RESULT 19
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Best Local Similarity 28.7%;
Matches 147; Conservative 8
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015767;
01-JAN-1998
01-JAN-1998
01-DEC-2001
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Eukaryota; Alveolata;
NCBI_TaxID=5866;
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STRAIN-MEXICO JG-29;
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                                                      KASSTGYKKFFKNILDTGAIKDAASRIGFPKK
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NCE 510 AA; 57468 MW;
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Pred. No. 9.2e-29;
0; Mismatches 177;
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Hotzel I., Suarez C.E., McElw
Submitted (SEP-1997) to the E
EMBL; AF014767; AAC47869.2; -
EMBL; AF014761; AAC47863.2; -
InterPro; IPR004318; RAP-1.
Pfam; PF03085; RAP-1; 1.
                                                                                                                                                                                                                                                            018684 PRELIMINARY;
018684 PRELIMINARY;
01-JAN-1998 (TREMBLEGL 0
01-JAN-1998 (TREMBLEGL 0
01-DEC-2001 (TREMBLEGL 1
     Pfam; PF03085;
NON_TER 191
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SEQUENCE 191
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Q9TVN0;
Q1-WAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Biochem. Parasitol. 90:479-483(1997).
EMBL; AF014758; AAC47870.2; -.
EMBL; AF014757; AAC47859.2; -.
EMBL; AF014758; AAC47860.2; -.
EMBL; AF014760; AAC47862.2; -.
EMBL; AF014762; AAC47864.2; -.
InterPro; IPB004318; RAP-1.
                                                                                                                                                                              Eukaryota; Alveolata;
NCBI_TaxID=5866;
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Eukaryota; Alveolata;
NCBI_TaxID=5866;
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                Babesia bigemina
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Hotzel I., Suarez C.E., McElwain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSASV 63
                                                                                                                                                                                                                                                                                                                                                                                                                               FENKLSFTTGLFGWG
                                                                                                                                                                                                                                                                                                                                                                                                                 FFNKLAFTTRLFGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEKRFW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEVVGDVSKTLLEANEVVNAEMEATQVNKDMQSQLSNVKETIVGEVCEKVAGNSTCGESV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRSR--SSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMTTLYYKTYLTVDFTAAK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAYVNRCDEGDCLTLDSM----
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191 AA;
191
191
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      AA;
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21574 MW;
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19,
                                                                                                                 McElwain T.F., Palmer the EMBL/GenBank/DDBJ
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Last sequence update)
Last annotation updat
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Pred. No. 8.4e-28;
2; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -KYKPLSLPNPYQLDAAFMLFRESDSNPAKNEVKRFW 118
                                                                                                                                                                                                                                                                                                                                 PRT;
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      E6666F1DE59CB26F CRC64;
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                                                                                                                   G.H.;
databases.
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Matches
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01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                  NON_TER
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Eukaryota; Alveolata;
NCBI_TaxID=5866;
                                                                                                                                                                                                                                                                                                                 Mol. Biochem. Parasitol. 90:479-489(1997). EMBL; AF014764; AAC47866.2; -. InterPro; IPR004318; RAP-1.
                                                                                                                                                                                                                                                                                                                                             MEDLINE-98135662; PubMed-9476795;
Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
"Genetic variation in the dimorphic regions of RAP-1
loci of Babesa bigemina.";
                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                 KLSFTTGLFGWG 198
                                                                                                         RRGKNHSYFHDLVFNLLEKNYTRDADATDIENFASRYLYMATLYYKTYTNVDEFGASFFN 186
                                                                                                                                                     MSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEKRFWMRF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAFTTRLFGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --SSHGDYHHFVYSLLKKNYVRDPESNDVENFASQYFYMTTLXYKTYLTVDFTAAKFFNK 180
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102; Conserv
                                                                                                                                                                                                                                                                         191
191 AA;
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Last sequence up
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Pred. No. 1.
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Pred. No. 5.2e-27;
 PRT;
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 219
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.8e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Babesiidae;
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015711;
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01-JAN-1998
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01-JAN-1998
01-DEC-2001
                                       Mol. Biochem. Parasitol. 90:479-483(1997).

EMBL; AF014765; AAC47867.2; -.

EMBL; AF014763; AAC47865.2; -.

EMBL; AF014766; AAC47868.2; -.

Interpro; IPR004318; RAP-1.

Pfam; PF03085; RAP-1; 1.

NON_TER 219 219
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Hotzel I., Suarez C.E., McElwain T.E.
"Genetic variation in the dimorphic
loci of Babesia bigemina.";
Mol. Biochem. Parasitol. 90:479-489(
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Eukaryota; Alveolata;
NCBI_TaxID⇒5866;
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                                                                                                                             MEDLINE-98135662; PubMed-9476795;
Hotzel I., Suarez C.E., McElwain T.F
"Genetic variation in the dimorphic
                                                                                                                                                                                                                             Ol-JAN-1998 (TrEMBLrel. O5, Created)
Ol-JAN-1998 (TrEMBLrel. O5, Last sequence update)
Ol-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RAP-1 BETA (RAP-1 ALPHA) (FRAGMENT).
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InterPro; IPR004318; RAP-1.
Pfam; PF03085; RAP-1; 1.
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                               SEQUENCE
                                                                                                                 loci of Babesia bigemina."
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                   Eukaryota; Alveo
NCBI_TaxID=5866;
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                                                                                                                                                                                                                                                                                                                                                                                                                          IAYVNRCDEGDCLTLDSM------KYKPLSLPNPYQLDAAFMLFRESDSNPAKNEVKCFW 146
                                                                                                                                                                                                                                                                                                                                                                                                                                    SAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDDYQLEAAFILFKESDANPANSTEKREW 123
                                                                                                                                                                                                                                                                                                                                                                                 MRSR--SSHGDYHHEVVSLLKKNVVRDPESNDVENFASQYFYMTTLYYKTYLTVDFTAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101;
Similarity
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(TrEMBLrel.
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                               24693 MW;
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21.7%;
51.8%;
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19,
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Last sequence update)
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Pred. No. 6.2e-27;
 Score
Pred.
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 513;
No. 1
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gions of RAP-1
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DB 5;
.8e-26;
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RAP-1
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01-MAR-2001 (TrEMBLrel. 16

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RAP1 BETA-3 (FRAGMENT).
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                                                                                                                                                                                                                                                                                              "Detection of equine antibodies to babesia caballi by caballi rhoptry-associated protein 1 in a competitive-enzyme-linked immunosorbent assay.";
J. Clin. Microbiol. 37:2285-2290(1999).
                                                                                                                                                                                                                                                                                                                        Kappmeyer L.S., Perryman L.E., Hines Hennager S.G., Knowles D.P.; "Detection of equine antibodies to be "Detection of equine antibodies to be
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  STRAIN-UYA;
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                                      Babesia bigemina
Eukaryota; Alveo
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                            NCBI_TaxID=5866;
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Eukaryota; Alveolata;
NCBI_TaxID=5866;
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Hotzel I., Suarez C.E., McElwain T.F.
"Genetic variation in the dimorphic
loci of Babesia bigemina.";
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Hotzel I., Suarez C.E., McElwain T.F.,
"Genetic variation in the dimorphic re
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EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN-GVRDLAR
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MEDLINE-98135662; PubMed-9476795;
Rocard I., Suarez C.E., McElwain T.F., Palme "Genetic variation in the dimorphic regions loci of Babesia bigemina.";
Mol. Biochem. Parasitol. 90:479-489(1997).
EMBL, AF017295; AAG14913.1; -.
                                      Eukaryota; Alveolata; NCBI_TaxID-5866;
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Mol. Blochem. Parasitol. 90.
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Interpro; IPRO04318; RAP-1.
Pfam; PF03085; RAP-1; 1.
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Hotzel I., Suarez C.E., McElwain T.F., Pall
"Genetic variation in the dimorphic region
loci of Babesia bigemina.";
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Hotzel I., Suarez C.E., McElwain T.F.,
"Genetic variation in the dimorphic reg
loci of Babesia bigemina.";
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Hotzel I., Suarez C.E., McElwain T.F., Palme
"Genetic variation in the dimorphic regions
loci of Babesia bigemina.";
Mol. Biochem. Parasitol. 90:479-489(1997).
EMBL; AF017294; AAG14912.1; -.
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Hotzel I., Suarez C.E., McElwain T.F.
"Genetic variation in the dimorphic
loci of Babesia bigemina.";
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50; Mismatches 85;
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STRAIN-PUERTO RICO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98135662; PubMed-9476795; Hotzel I., Suarez C.E., McElwain "Genetic variation in the dimorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            loci of Babesia bigemina.";
Mol. Biochem. Parasitol. 90:479-489(1997).
EMBL; AF017290; AAG14908.1; -.
EMBL; AF017285; AAG14903.1; -.
EMBL; AF017286; AAG14904.1; -.
EMBL; AF017288; AAG14906.1; -.
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                                                                                                                                STRAIN-CGA;
MEDLINE-98135662;
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Eukaryota; Alveolata;
NCBI_TaxID=5866;
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Mol. Biochem. Parasitol. 90
EMBL; AF017284; AAG14902.1;
                                                                                           MEDLINE=98135662; PubMed=9476795;
Hotzel I., Suarez C.E., McElwain T.I
"Genetic variation in the dimorphic
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Eukaryota; Alveolata;
NCBI_TaxID=5866;
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Hotzel I., Suarez C.E., McElwain T.F.,
"Genetic variation in the dimorphic re-
loci of Babesia bigemina.";
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Best Local S
Matches 113
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16
RAP-1 ALPHA-1 (FRAGMENT).
RAP-1 ALPHA-1.
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STRAIN-PUERTO RICO;
MEDLINE-98135662; PubMed-9476795;
Hotzel I., Suarez C.E., McElwain T.F., Palme
"Genetic variation in the dimorphic regions
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Eukaryota; Alveolata; Apicomplexa;
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Blochem. Parasitol. 90:479-489(1997).
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Pred. No. 6.4
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Best Local Similarity
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                                                                                                                                     Q17258;
Q17258;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 11,
01-DEC-2001 (TrEMBLrel. 19,
RHOPTRY PROTEIN (FRAGMENT).
          STRAIN-ANKARA;
MEDLINE-93165069; PubMed-8433711;
Dalrymple B.P., Casu R.E, Peters
Wright I.G.;
                                                                                                        01-NOV-1996 (TREMBLIEL 01, 01-NOV-1996 (TREMBLIEL 01, 01-DEC-2001 (TREMBLIEL 19,
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Dalrymple B.P., Casu R.E.,
Bose R., Wright I.G.;
Submitted (AUG-1992) to the
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Eukaryota; Al
                                                                 викагуота; Alveolata;
NCBI_TaxID=5869;
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                                                                                       Babesia ovis
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  "Characterisation of a
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Pred. No. 1.5e-19;
0; Mismatches 29
 of multi-copy
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                                                                            Piroplasmida;
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Matches 69
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                                 01-MAY 1997 (TIEMBLIEL 0:
01-MAY-1997 (TIEMBLIEL 0:
01-NOV-1998 (TIEMBLIEL 0:
BCAB60 (FRAGMENT).
Babesia caballi.
Eukaryota; Alveolata; Api
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096431;
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SEQUENCE
                                                                                                                 P90650;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence upda
01-MAY-1999 (TrEMBLrel. 10, Last annotation up
PUTATIVE MEROZOITE SURFACE PROTEIN (FRAGMENT).
Babesia cabali.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein homologues in Babesia bovis, Babesia ovis and Babesia canis."; Mol. Biochem. Parasitol. 57:181-192(1993).

EMBL; M91173; AAA27812.1; -.

Interpro; IPR004318; RAP-1.

Pfam; PF03085; RAP-1; 1.
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                    NCBI_TaxID=5871;
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SEQUENCE FROM N.A.
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69 AA;
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nilarity 43.3%;
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7792 MW;
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                                     Apicomplexa; Piroplasmida; Babesiidae;
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Pred. No. 8.4e-17;
0; Mismatches 59;
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SEQUENCE
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Dalrymple B.P., Peters J.M., Bose R., Wright I.G.;
"A polymerase chain reaction method for the identification of genes encoding members of the Bv60/p58 family of rhoptry protein homologues In the genus Babesia.";
In the genus Babesia.";
Exp. Parasitol. 84:96-100(1996).
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                                                                                                                         104 FILFKESDANPANSTEKRFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRY 163
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62 AA;
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                October 19,
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7507 MW;
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